

22. A transgenic plant cell comprising the recombinant expression cassette of claim 5.

A4 23. The transgenic plant cell of claim 22 wherein the promoter sequence and the polyadenylation signal sequence is from Cauliflower Mosaic Virus 35S gene.

Please delete claims ~~24~~ and ~~13-21~~ without prejudice.

IN THE SPECIFICATION:

On page 1, line 3, insert the following:

"RELATED APPLICATION INFORMATION

A5 The instant application is a 371 of PCT/US00/2000, which claims priority to U.S. Provisional Applications 60/169,858 filed on December 9, 1999 and 60/123,888 filed on March 11, 1999."

[Please amend page 15, lines 20-22 as follows:] "FIG. 1A shows the nucleic acid sequence of the zmet2a methyltransferase gene containing 2736 basepairs (SEQ ID NO:1). FIG. 1B shows the nucleic acid sequence of the zmet2a methyltransferase gene containing 2796 basepairs (SEQ ID NO:2).

A6 [Please amend page 15, lines 24-28 as follows:] "FIG. 2A shows the amino acid sequence of the zmet2a methyltransferase containing 912 amino acids and which is encoded by the nucleic acid sequence shown in FIG. 1A (SEQ ID NO:3). FIG. 2B shows the amino acid sequence of the zmet2a methyltransferase containing 932 amino acids and which is encoded by the nucleic acid sequence shown in FIG. 1B (SEQ ID NOS:4 and 5)."

[Please amend page 15, lines 30-31 as follows:] "FIG. 3 shows the PCR primers used to sequence the zmet2a methyltransferase gene (SEQ ID NOS: 6-42)."

A7 [Please amend page 15, lines 36-38 as follows:] "FIG. 5 shows the genomic sequence of zmet2a methyltransferase gene and the retrotransposon SPRITE-1, along with intron-exon divisions, a restriction site map and a primer map (SEQ ID NO:90).

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Please amend page 16, lines 11-24 as follows: FIG. 8 shows the alignment of the amino acid sequence from zmet2a (SEQ ID NO:43) with the amino acid sequence of [*Arabidopsis*] *Arabidopsis* chromomethylase *CMT1* (AF039367) (SEQ ID NO:44) and the C-terminal methylase domains from the DNA methyltransferases of maize zmet1 (AF063403) (SEQ ID NO:45) and *Arabidopsis* *MET1* (P34881) (SEQ ID NO:46). Zmet2a shows similarity along the entire length of *CMT1* but significant similarity with zmet1 and Met1 exists only in the conserved motifs. Bold, uppercase, normal uppercase letters, and lower case letters indicate identity, conservation and differences in amino acid sequences relative to zmet2a respectively. Dashes in the sequence are gaps introduced by CLUSTAL W to optimize the alignments. The location of the six conserved methylase motifs are indicated in the sequence. The chromodomain is located upstream and adjacent to motif IV. The *Mu* insertion into the coding region of motif IX alters zmet2a function resulting in decreased methylation at CpNpG sites. Putative nuclear [localization] localization signal peptides, NLS (N. Raikhel, *Plant Physiol.* 100, 1627 (1992)) are positioned in the N-terminal portion of the protein."

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Please amend page 19, lines 4-12 as follows: FIG. 16 shows [the structure of maize retrotransposon SPRITE-1 and sequence of Long Terminal Repeat (hereinafter "LTR") components. FIG. 16A shows that SPRITE-1 consists of long terminal direct repeats, a tRNA primer binding site (hereinafter "PBS"), coding sequence for proteins necessary for replication and transposition, and a polypurine tract (hereinafter "PPT"). FIG. 16B identifies] the sequences for the 5' and 3' Long Terminal Repeats ( hereinafter "LTR"), primer binding site (hereinafter "PBS") (SEQ ID NO:47) and polypurine tract (hereinafter "PPT") (SEQ ID NO:48). Each LTR has a 3 base pair inverted repeat which is also shown in the drawing. A putative TATA box is underlined and the putative transcription start site is italicized. The 5 base pair host insertion site duplications are also identified."

Please amend page 19, lines 14-18 as follows: FIG. 17 shows the alignments of the conserved protein motifs of the Ty1/copia elements with SPRITE-1. The maize retrotransposon SPRITE-1 (SEQ ID NOS: 49, 50, 59, 64, 65, 74 and 75) is aligned with the retrotransposon hotscotch (U2626) (SEQ ID NOS: 51, 52, 60, 66, 67, 76 and 77) from [maizze] maize, retrofit (U72725) (SEQ ID NOS: 53, 54, 61, 68, 69, 78 and 79) from rice, an unpublished *Arabidopsis* retrotransposon (AC006528) (SEQ ID NOS: 55, 56, 62, 70, 71, 80 and 81) and the copia element from *Drosophila* (M11240) (SEQ ID NOS: 57, 58, 63, 72, 73, 82 and 83)."

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Q10 Please amend page 21, lines 4-5 as follows: "FIG. 23 shows partial nucleic acid sequence of the zmet2b methyltransferase gene (SEQ ID NO:84)."

Q11 Please amend page 21, lines 7-8 as follows: "FIG. 24 shows a partial amino acid sequence of the zmet2b methyltransferase (SEQ ID NOS: 85 and 86) encoded by the partial nucleic acid sequence shown in FIG. 23 (SEQ ID NO:84)."

Q12 Please amend page 21, lines 10-12 as follows: "FIG. 25 shows a comparison of a portion of the amino acid sequence for zmet2a methyltransferase (SEQ ID NO:87) with a portion of the amino acid sequence for zmet2b methyltransferase (SEQ ID NO:89). The amino acid sequence shown in between the portion of the amino acid sequence for zmet2a methyltransferase and the portion of the amino acid sequence for zmet2b methyltransferase identifies the common amino acids between the two sequences (see SEQ ID NO:88)."

Q13 Please amend page 41, lines 10-19 as follows: "Sequence of zmet2a (FIG. 1A and 1B) reveals that it lacks the large N-terminal domain found in the maintenance enzymes but does possess the six highly conserved motifs of the C-terminal catalytic domain. Database searches using BLAST [<http://www.ncbi.nlm.nih.gov/gov/BLAST/>]) show that zmet2a has highest sequence homology to the *Arabidopsis* chromomethylase, *CMT1* (see Henikoff and Comai, *Genetics*, 148:307-318 (1998)) with 44% identity, 57% conservation. The N-terminal region is larger in zmet2a; however, there is an additional downstream predicted start site, also within a consensus Kozak sequence, that codes for an enzyme of 809 amino acids which is more similar in size to the most closely related *CMT1* which is composed of 791 amino acids."

Q14 Please amend pages 53, beginning at line 28 through page 54, line 4 as follows: "Database searches for similar coding sequences using BLAST [<http://www.ncbi.nlm.nih.gov/gov/BLAST/>]) show that SPRITE-1 belongs to a different family of retroelements than any other previously described. The most closely related elements based on overall amino acid similarity include an *Arabidopsis* retroelement (AC006528), Retrofit from *Orzya longstaminata* (U72725), and Hopscotch from *Zea mays* (U12626) all having ~35% identity and ~50% conservation in amino acid sequence with SPRITE-1. It also shares 29% identity and 45% conservation with the *copia* elements from *Drosophila*. No elements were found to have nucleotide similarity with the LTR of SPRITE-1 further indicating that this is a member of a unique family of Ty1/*copia* type elements."

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